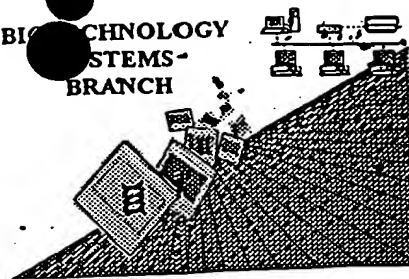




RAW SEQUENCE LISTING ERROR REPORT

BIO TECHNOLOGY
SYSTEMS-
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 763 011A
Source: PCT 09
Date Processed by STIC: 11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/763011A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(i) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(iii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

**Does Not Comply
Corrected Diskette Needed**

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5 <110> APPLICANT: Contreras, Roland
6   Nelissen, Bart
7   DeBacker, Marianne
8   Luyten, Walter
9   Viaene, Jasmine
10  Logghe, Marc George
13 <120> TITLE OF INVENTION: Drug Targets In Candida Albicans
16 <130> FILE REFERENCE: 50899/002
-> 19 <140> CURRENT APPLICATION NUMBER: US/09/763,011A 0K
-> 21 <141> CURRENT FILING DATE: 2001-02-14
24 <150> PRIOR APPLICATION NUMBER: 98310694.9
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RAW SEQUENCE LISTING

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DATE: 11/14/2001

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RAW SEQUENCE LISTING

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DATE: 11/14/2001

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238 20 25 30
242 Ile Ser Ile Leu Thr Asn His Phe Gln Ile Leu Lys Asp Leu Leu Pro
244 35 40 45
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250 50 55 60
254 Lys Val Ser Arg Asp Gly Val Pro Ile Asn Phe His Arg Ala Pro Ala
256 65 70 75 80
260 Ile Ile Met Lys Ser Asn Lys Thr Asp Asp Leu Val Arg Asn Ser Asn
262 85 90 95
266 Lys Thr Met Val Leu Thr Glu Ile Lys Thr Ile Thr Glu Phe Ala Thr
268 100 105 110
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328 260 265 270
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334 275 280 285
338 Ala Thr Lys Thr Glu Val Ala Tyr Met Lys Pro Lys Ile Val Trp Thr
340 290 295 300
344 Asn Phe Pro Thr Thr Thr Ala Thr Ser Met Phe Asp Asn Phe Ile Leu
346 305 310 315 320
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001

TIME: 13:52:05

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Output Set: N:\CRF3\11142001\I763011A.raw

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368 Ser Glu Leu Gly Thr Lys Thr Pro Asn Phe Glu Asp Pro Phe Glu Gln
370          370          375          380
374 Ile Asn Ile Glu Asp Asn Lys Val Ile Ser Val Asn Thr Pro Lys Thr
376 385          390          395          400
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388          420          425          430
392 Arg Arg Lys Gln Ser Ser Ser Phe Lys Asn Lys Asn Ser Thr Ile Lys
394          435          440          445
398 Phe Asp Val Phe Asp Trp Ile Phe Glu Ser Gly Thr Thr Asn Glu Lys
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001

TIME: 13:52:05

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532 35 40 45
536 Glu Ile Asn Ile Ala Tyr Glu Thr Ile Arg Asp Tyr Tyr Gln Glu Asn
538 50 55 60
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568 130 135 140
572 Lys Lys Glu Leu Phe Gln Arg Gln Gln Ala Glu Glu Ala Gln Arg Lys
574 145 150 155 160
578 Lys Glu Phe Glu Gln Lys Ala Glu Phe Ile Lys Ala Ser Leu Leu Glu
580 165 170 175
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590 Gln Arg Gln Lys Glu His Glu Ala Lys Arg Asp Ile Arg Ile Gln Gln
592 195 200 205
596 Leu Ser Glu Gln Asp Ser Arg Ser Asn Gln Thr Lys Glu Glu Glu Glu
598 210 215 220
602 Val Phe Lys Lys Ala Arg Ser Thr Asn Ser Gly Ala Asp Glu Thr Gly
604 225 230 235 240
608 Leu Met Ser Asp Lys Glu Phe Asp Asp Ser Ala Tyr Ser Pro Asp Tyr

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09/763011A

Page 5 of 7B

210> 13

211> 302

212> PRT

213> Candida albicans

220>

221> Xaa = any amino acid at positions 58 and 185

Does Not Comply
Corrected Diskette Needed

1. Unknowns must be enumerated in fields 221 222 and 223,
2. Field 221 as "variant"
3. Field 222 as location "58 and 185"
4. Field 223 as particular amino proteins

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001

TIME: 13:52:06

Input Set : A:\JAB-1415.txt

Output Set: N:\CRF3\11142001\I763011A.raw

19 M:270 C: Current Application Number differs, Replaced Application Number
21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
1041 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
1067 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
1067 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
1115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
1115 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
1115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
5512 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:57
5742 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:57
5742 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:57
5742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
5789 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58
6635 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:58
6635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:58
6635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
13167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:114
13330 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
13330 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
13330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114
13348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
13348 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
13348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114